c/c

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/662,358	09/16/2003	Sang Yup Lee	Q77446	2373

23373	7590	06/02/2005

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EXAMINER
WALICKA, MALGORZATA A

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 06/02/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

		Application No.	Applicant(s)
Office Action Summary		10/662,358	LEE ET AL.
		Examiner	Art Unit
		Malgorzata A. Walicka	1652

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) FROM
THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed
  after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any
  earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>29 April 2005</u>.

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is
closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-10* is/are pending in the application.

4a) Of the above claim(s) <u>4</u> is/are withdrawn from consideration.

5)☒ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3 and 5-10* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All   b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage
application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____.

4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ .

5) ☐ Notice of Informal Patent Application (PTO-152)

6) ☒ Other: *See Continuation Sheet*.

Continuation of Attachment(s) 6). Other: sequence alignment used in 102 and 103 rejections.

Response to Restriction Requirement filed April 29, 2005 is acknowledged. Claims 1-10 are pending. Claims 1-3 and 5-10, drawn to *maoC* gene, expression vectors, host cells and a method of production of middle-chain-length polyhydroxyalkanoate are under examination. Claim 4 is withdrawn from Examiner's consideration as drawn to a nonelected invention; see 37 CFR 1.142(b).

DETAIL ACTION

1. Restriction/election

Applicant's election, with traverse, of the invention of Group I, claims 1-3 and 5-8 is acknowledged. The traversal is on the ground that Group I and Group III should be examined together because the justification of restriction between Group I and III is improper.

Applicants' argument is fully considered and persuasive. The restriction as written contains typographical error that makes it incorrect. The method as claimed in Group III can be only practiced using the product of Group I. Thus, the restriction between Group I and III is withdrawn, and both Groups, i.e., claims 1-3 and 9-10 are examined together. Restriction between the new Group I, claims 1-3 and 5-10, and Group II, claim 4, is proper for the reasons explained in the restriction requirement and therefore made FINAL.

2. Priority

The priority to the Korean Application 10-2003-0025863 is noted and granted. The priority document is acknowledged.

3. Objections

3.1. Specification

The specification is objected to for lack, in the first sentence, of a reference to the priority document.

The specification comprises sentences that are not in improper idiomatic English, for example page 1, line 20, to the end of the paragraph. Applicants are requested to correct the improperly written passages.

The specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors in the specification of which applicant may become aware.

3.2. Claims

Claim 7 objected to for reciting the phrase "a synthase gene is cloned into a chromosome". In the context used one should say "integrated" and not "cloned".

4. Rejections

4.1. 35 USC section 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claim 1-3 and 5 are rejected under 35 U.S.C. 102(b) as being anticipated by Ferrandez et al. (Catabolism of Phenylacetic acid in *Escherichia coli*, J. Biol. Chem. 1998, 273, 25974-25986).

The claims are directed to

(1)   the *maoC* gene of SEQ ID NO: 2 encoding the enzyme of SEQ ID NO: 1 showing enoyl-CoA hydratase activity providing monomers required for the synthesis of middle-chain-length polyhydroxalkanoate,

(2)   a recombinant vector containing gene (1), and

(3)   a microorganism transformed with the recombinant vector (2).

Ferrandez et al. disclose the gene (*paaZ*) encoding protein identical to SEQ ID NO: 1 of the instant invention (see the alignment of the nucleotide and amino acid sequences). Ferrandez et al. teach "the paaZ gene caused the conversion of PA [phenyl acetic acid] into a metabolite whose retention time in HPLC was identical to that of standard 2-HPA. Gas chromatography–mass spectrometry analysis confirmed this metabolite as 2-HPA [2-hydroxyphenylacetate formed in result of action of enoyl-CoA hydratase]", page 25978, left column, second paragraph. Ferrandez et al. express said

gene in *E. coli* for sequencing purposes, see page 25975, left column, subtitle *"DNA Manipulation and Sequencing"*. In conclusion, Ferrandez et al disclosed an invention identical to that claimed by Applicants in claims 1-3 and 5.

In addition, claim 1 and 2 are rejected as anticipated by DNA molecule accession No. AB001340, open to the public 29 May, 1997, encoding enoyl–CoA hydratase; see the enclosed sequence alignment.

4.3. 35 USC section 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claim 6-10 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ferrandez et al. (Catabolism of Phenylacetic acid in *Escherichia coli*, J. Biol. Chem. 1998, 273, 25974-25986) in view of a common knowledge in biotechnology and in view of Tsuge et al. (Molecular cloning of two (*R*)-specific enoyl-CoA hydratase genes from

Pseudomonas aeruginosa and their use for polyhydroxyalkanoate synthesis, FEMS Microbiology Letters,1999, 189, 193-198).

The claims are directed to:

a)   a microorganism transformed with the *MaoC* gene of E. coli wherein the *fadB* gene is deleted and a gene containing PHA synthase is introduced,

b)   the microorganism as in a) wherein the PHA synthase gene is incorporated into a chromosome.

c)   the a) microorganism wherein the PHA synthase gene is *phaC*, and

d)   a method of producing MCL-PHA comprising culturing transfomant a).

Ferrandez et al. teach the *maoC* gene of E. coli identical to the one claimed in the instant claims, but Ferrandez et al. do not teach production of MCL-PHA as in d).

Tsuge et al. teach production of MCL-PHA in E. coli, having *fadB* gene deleted and harboring $phaC_{Ac}$ gene of *A. caviae* having the same function, i.e., encoding PHA synthase, wherein said *E. coli* transformant is additionally transformed with *Pseudomonas aeruginosa* gene $phaJ2_{Pa}$ encoding enoyl–CoA hydratase for providing monomers for synthesis of MCL- PHA; see section 2. Materials and methods and Table 3, page 196.

It would have been obvious to one having ordinary skill in the art at the time of invention to have an *E. coli* transformant of Tsuge et al. and replace the *Pseudomonas aeruginosa* gene for production monomers required for the synthesis of MCL-PHA, with a gene that originates from *E.coli* itself, i.e., the gene taught by Ferrandez et al. It would also have been obvious to use such transformant for production of MCL-PHA.   The

expectation of success was very high taking into account a routine character of the genetic manipulations with *E. coli.* The motivation to replace *Psequdomonas aeruginsa* gene with that of *E. coli* would been to obtain the more efficient producer of MCL-PHA than that of Tsuge, because one of skills in the art realizes that expression of *E. coli* gene in *E. coli* is more efficient than expression of *Pseudomonas gene* in *E.coli,* and in result, the production of MCL-PHA should be more efficient.

Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

5. Conclusion

All claims are rejected.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Malgorzata A. Walicka whose telephone number is (571) 272-0944. The examiner can normally be reached on Monday-Friday from 10:00 a.m. to 4:30 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura Achutamurthy, can be reached on (571) 272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for

published applications may be obtained from either Private PAIR or Public PAIR.

Status information for unpublished applications is available through Private PAIR only.

For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic

Business Center (EBC) at 866-217-9197 (toll-free).

Malgorzata A. Walicka, Ph.D.

Art Unit 1652

Patent Examiner

PONNATHAPU ACHUTAMURTHY
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 20:50:45 ; Search time 91 Seconds.
                                         (without alignments)
                                         3832.153 Million cell updates/sec

Title: US-10-662-358-1
Perfect score: 3489
Sequence: 1 MQQLASFLSGTWQSGRGRSR..........PVALYSILTLVARQHGDFVD 681

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt.03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3489	100.0	681	1	MAOC_ECOLI	P77455 escherichia
2	1984	56.9	684	2	Q84570	pseudomonas
3	1984	56.9	688	2	Q84987	pseudomonas
4	1956	56.1	684	2	Q88HT3	pseudomonas
5	1953	56.0	700	2	Q9RRV4	pseudomonas
6	1950	55.9	684	2	Q70IL3	deinococcus
7	1817.5	52.1	669	2	Q92TG5	rhizobium m
8	1702.5	48.8	668	2	Q72K14	thermus the
9	1633.5	46.8	679	2	Q6N925	rhodopseudo
10	1578.5	45.2	705	2	Q6RT1	corynebacte
11	1402	40.2	335	1	MAOC_KLEAE	P92251 klebsiella
12	978.5	28.0	515	2	Q8FRT1	corynebacte
13	396	11.3	509	2	Q84HH8	azoarcus ev
14	378.5	10.7	509	2	Q9K3J2	streptomyce
15	372.5	10.7	476	2	Q82H84	streptomyce
16	357	10.2	454	2	Q88Z20	pseudomonas
17	349.5	10.0	490	2	Q8PJR1	xanthomonas
18	344	9.9	484	2	Q8PPG7	xanthomonas
19	344	9.9	490	2	Q59095	yersinia pe
20	344	9.8	496	2	Q82GV9	acinetobact
21	343	9.8	496	2	Q99R24	staphylococ
22	343	9.8	496	2	Q792X3	staphylococ
23	343	9.8	496	2	Q7A399	staphylococ
24	343	9.8	496	2	Q914P8	staphylococ
25	342.5	9.8	493	2	Q9G663	staphylococ
26	342	9.8	490	2	Q73TQ6	mycobacteri
27	337	9.7	490	2	Q6GDJ0	staphylococ
28	336	9.6	477	2	Q6DS3	yersinia ps
29	336	9.6	490	2	Q8KJG2	rhizobium l
30	336	9.6	498	2	Q65FG8	bacillus li
31	335.5	9.6	490	2	Q62R67	bacillus li
32	335.5	9.6	495	2	Q8P5D8	xanthomonas
33	333	9.5	481	2	Q9RZ27	deinococcus
34	333	9.5	497	2	Q98A95	rhizobium 1
35	332	9.5	454	2	Q9X2M1	staphylococ
36	331.5	9.5	491	2	Q8KP43	xanthomonas
37	330.5	9.5	485	2	Q8P8A7	pseudomonas
38	330.5	9.5	496	2	Q6NER7	corynebacte
39	329.5	9.4	525	2	Q6SF25	uncultured
40	329.5	9.4	493	2	Q8CMY1	staphylococ
41	329	9.4	475	2	Q9K7P5	xanthomonas
42	329	9.4	503	2	Q6NDJ3	rhodopseudo
43	328	9.3	487	2	Q8PGH1	rhodopseudo
44	325.5	9.3	487	1	P96405	mycobacteri
45	325.5	9.3	523	2	XYLC_PSEPU	Q74ZT0 mycobacteri

ALIGNMENTS

```
RESULT 1
MAOC_ECOLI                                   STANDARD;    PRT;    681 AA.
ID   MAOC_ECOLI
AC   P77455; O53009;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   MaoC protein (Phenylacetic acid degradation protein paaZ).
GN   Name=maoC; Synonyms=paaZ; OrderedLocusNames=b1387;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97251357; PubMed=9097039;
RA   Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA   Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA   Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA   Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA   Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA   Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT   "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 28.0-40.1 min region on the linkage map.";
RL   DNA Res. 3:363-377(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W / ATCC 11105;
RX   MEDLINE=98421522; PubMed=9748275; DOI=10.1074/jbc.273.40.25974;
RA   Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,
RA   Garcia J.L., Diaz E.;
RT   "Catabolism of phenylacetic acid in Escherichia coli. Characterization
RT   of a new aerobic hybrid pathway.";
RL   J. Biol. Chem. 273:25974-25986(1998).
RN   [4]
RP   TRANSCRIPTIONAL REGULATION.
RX   MEDLINE=20229831; PubMed=10766858; DOI=10.1074/jbc.275.16.12214;
RA   Ferrandez A., Garcia J.L., Diaz E.;
RT   "Transcriptional regulation of the divergent paa catabolic operons for
RT   phenylacetic acid degradation in Escherichia coli.";
RL   J. Biol. Chem. 275:12214-12222(2000).
-!- PATHWAY: Phenylacetic acid aerobic catabolism.
-!- INDUCTION: Activated by cAMP receptor protein (CRP) and
```

```
CC        integration host factor (IHF). Inhibited by paaX.
CC   -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
CC   ------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------
DR   EMBL; X97452; CAA66089.1; -.
DR   EMBL; U00096; AAC74469.1; -.
DR   EMBL; D90777; BAA14997.1; -.
DR   PIR; F64889; F64889.
DR   EchoBASE; EB3498; -.
DR   EcoGene; EG13735; maoC.
DR   InterPro; IPR002086; Aldehyde dehydr.
DR   InterPro; IPR002539; MaoC dehydratas.
DR   Pfam; PF00171; Aldedh; 1.
DR   Pfam; PF01575; MaoC dehydratas; 1.
DR   PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; FALSE_NEG.
KW   Complete proteome; Oxidoreductase.
FT   ACT_SITE    256    256    By similarity.
FT   ACT_SITE    295    295    By similarity.
FT   VARIANT     143    143    L -> V (in strain W).
FT   VARIANT     440    440    A -> T (in strain W).
FT   VARIANT     611    611    S -> N (in strain W).
SQ   SEQUENCE   681 AA;  73002 MW;  A631B97AA37A1C3E CRC64;

Query Match            100.0%;  Score 3489;  DB 1;  Length 681;
Best Local Similarity  100.0%;  Pred. No. 2.9e-220;
Matches  681;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  MQQLASFLSGTWQSGRGRSRLIHHAISGEALWEVTSEGLDMAAARQFAIEKGAPALRAMT  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MQQLASFLSGTWQSGRGRSRLIHHAISGEALWEVTSEGLDMAAARQFAIEKGAPALRAMT  60

Qy     61  FIERAAMLKAVAKHLLSEKERFYALSAQTGATRADSWVDIEGGIGTLFTYASIGSRELPD  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  FIERAAMLKAVAKHLLSEKERFYALSAQTGATRADSWVDIEGGIGTLFTYASIGSRELPD  120

Qy    121  DTLWPEDELIPLSKEGGFAARHLLTSKSGVAVHINAFNPPCWGMLEKLAPTWLGGMPAII  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DTLWPEDELIPLSKEGGFAARHLLTSKSGVAVHINAFNPPCWGMLEKLAPTWLGGMPAII  180

Qy    181  KPATATAQLTQQAMVKSIVDSGLVPEGAISLICGSSAGDLLDHLDSQDVVTFGSSAATGQML  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  KPATATAQLTQQAMVKSIVDSGLVPEGAISLICGSSAGDLLDHLDSQDVVTFGSSAATGQML  240

Qy    241  RVQPNIVAKSIPFTMEADSLNCCVLGEDVTPDQPEFALFIREVVREMTTKAGQKCTAIRR  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  RVQPNIVAKSIPFTMEADSLNCCVLGEDVTPDQPEFALFIREVVREMTTKAGQKCTAIRR  300

Qy    301  IIVPQALVNAVSDALVARLQKVVVGDPAQEGVKMGALVNAEQRADVQEKVNILLAAGCEI  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  IIVPQALVNAVSDALVARLQKVVVGDPAQEGVKMGALVNAEQRADVQEKVNILLAAGCEI  360

Qy    361  RLGGQQADLSAAGAFPPTLLYCPQPDETPAVHATEARGPVATLMPAQNQRHALQLACAGG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  RLGGQQADLSAAGAFPPTLLYCPQPDETPAVHATEARGPVATLMPAQNQRHALQLACAGG  420

Qy    421  GSLAGTLVTADPQIARQFIADAARTHGRIQILNEESAKESTCHGSPLPQLVHGGPGRAGG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GSLAGTLVTADPQIARQFIADAARTHGRIQILNEESAKESTCHGSPLPQLVHGGPGRAGG  480

Qy    481  GEELGGLRAVKHYMQRTAVQQGSPTMLAAISKQWVRGAKVEEDRIHPFRKYFEELQPGDSL  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GEELGGLRAVKHYMQRTAVQQGSPTMLAAISKQWVRGAKVEEDRIHPFRKYFEELQPGDSL  540

Qy    541  LTPRRTMTEADIVNFACLSGDHFYAHMDKIAAAESIFGERVHGYFVLSAAAGLFVDAGV  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  LTPRRTMTEADIVNFACLSGDHFYAHMDKIAAAESIFGERVHGYFVLSAAAGLFVDAGV  600

Qy    601  GPVIANYGLESLRFIEPVKPGDTIQVRLTCKRKTLKKQRSAEEKPTGVVEWAVEVFNQHQ  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GPVIANYGLESLRFIEPVKPGDTIQVRLTCKRKTLKKQRSAEEKPTGVVEWAVEVFNQHQ  660

Qy    661  TPVALYSIILTLVARQHGDFVD  681
           ||||||||||||||||||||||
Db    661  TPVALYSIILTLVARQHGDFVD  681
```

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RESULT 2
Q84J50
ID   Q84J50          PRELIMINARY;    PRT;   684 AA.
AC   Q84J50;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative ring-opening enzyme.
GN   Name=paaN;
OS   Pseudomonas sp. Y2.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=198931;
RN   [1]
RP   SEQUENCE FROM N.A.
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RA   Garcia J.L.;
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98155131; PubMed=9495743;
RA   Velasco A., Alonso S., Garcia J.L., Perera J., Diaz E.;
RT   "Genetic and functional analysis of the styrene catabolic cluster of
RT   Pseudomonas sp. strain Y2.";
RL   J. Bacteriol. 180:1063-1071(1998).
DR   EMBL; AJ000330; CAD76942.1; -.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002086; Aldehyd_dehydrog.
DR   Pfam; PF00171; Aldedh; 1.
SQ   SEQUENCE   684 AA;  72859 MW;  ABCC5AF37CE77882 CRC64;

Query Match            56.9%;  Score 1984;  DB 2;  Length 684;
Best Local Similarity  59.1%;  Pred. No. 1.5e-121;
Matches  401;  Conservative   84;  Mismatches  185;  Indels   8;  Gaps   4;

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Db      7  LQSFIGGRWIGQQG--AQALRSALDGHRTVARFIHEETLDFTEAVEHGRRHGIAALMANDFQQ   65

Qy     64  RAAMLKAVAKHLLSEKERFYALSAQTGATRADSWVDIEGGIGTLFTYASIGSRELPDTTL  123
           |||:|||:.|:|||:|:::|| ||:.|||||||||||||| |||| :||:|::||| . :
Db     66  RAARLKALGKILSERKEQLYAISHHSGATRADSWVDIEGGAGTLFAVASLGARELPSGNV  125

Qy    124  WPEDELIPLSKEGGFAARHLLTSKSGVAVHINAFNPPCWGMLEKLAPTWLGGMPAIIKPA  183
           ||| |||||.||.||:|.|:||. ||||||||||||| |||| |.|| :|.|||| |||
Db    126  VHEGPALPLGKTNKFAGSHILVPRGGVAVHINAFNPIPWGMLASHAQQADVAARVETLL  185

Qy    184  TATAQLTQQAMVKSIVDSGLVPEGAISLICGSSAGDLLDHLDSQDVVTFGSSAATGQMLRVQ  243
           ::: |:|: |:::|:::|||:|.|:|.|| || .|||||.| .|||||||||||:|..|||
Db    184  TSYITEAAVRLMHESGLLPAGSLQLIIGGTGDLLDRLQGGDVDVVTFGSSADTAARLRVN  245

Qy    244  PNIVAKSIPFTMEADSLNCCVLGEDVTPDQPEFALFIREVVREMTTKAGQKCTAIRRIIV  303
           .|:|...||| .||||||| :|..|:||| .||.||:.||.||||||||||||||||.||
Db    246  ANLVRNSIPFNAEADSLNCAILAPEITPDDSEFDLFVKEVAREMTTKAGQKCTAIRRAIV  305

Qy    304  PQALVNAVSDALVARLQKVVVGDPAQEGVKMGALVNAEQRADVQEKVNILLAAGCEIRLG  363
           |:|:::||::.|.|||.|||||||: |||||||| .:.|:||| :.|.|||.||.:||.|
Db    306  PARYIDAVAERLHARLAKVVVGDPSVEGVKMGALASHAQQADVAARVETLL---AGSDLLFG  364

Qy    364  ---GQADLS----AAGAFPPTLLYCPQPDETPAVHATEARGPVATLMPAQNQRHALQLAC  417
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Db    365  ARDGFAPLGEGVAEGAPFAPTLLRSRDPHAEGGADIEARGPVSTLMAYDLDRAIALAA  424
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: May 20, 2005, 17:14:38 ; Search time 8749 Seconds
                 (without alignments)
                 11331.509 Million cell updates/sec

Title: US-10-662-358-2
Perfect score: 2046
Sequence: 1 atgcagcagttagccagtt.........acggtgatttgtcgattaa 2046

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 4708233 seqs, 2422607955 residues
Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :   GenEmbl:*
                 1: gb_ba:*
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                 8: gb_pl:*
                 9: gb_pri:*
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                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2046	100.0	18554	1	D90777	D90777 E.coli geno
2	2046	100.0	110000	1	U00096_14	Continuation (15 o
3	2020.4	98.7	14328	1	ECPAA	X97452 E.coli paa
4	1237.6	60.5	2064	6	AR390037	AR390037 Sequence
5	737.6	36.1	20878	2	AC137548	AC137548 Macaca mu
6	720.4	35.2	4124	1	KPNMAOAC	D10208 K. aerogene
7	659.2	32.2	214921	2	AC146130	AC146130 Pan trogl
8	641.2	31.3	29685	1	PSSTYCATA	AJ000330 Pseudomon
9	636.6	31.1	21562	1	PSP579894	AJ579894 Pseudomon
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12	614.8	30.0	10831	1	AE002069	AE002069 Deinococc
13	588.2	28.7	2118	6	AR320003	AR320003 Sequence
14	551.4	27.0	34879	1	RME591985_16	BX572598 Rhodopseu
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16	443.6	21.7	27418	1	AE017303	AE017303 Thermus t
17	411.6	20.1	2004	6	BD180143	BD180143 Highly th
18	410	20.0	308750	1	AP005216	AP005216 Corynebac
19	377.2	18.4				

c 20	373.4	18.3	219014	2	AC024141	AC024141 Mus muscu
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c 22	204.8	10.0	354	6	AR389923	AR389923 Sequence
c 23	161.2	7.9	246	6	AR390017	AR390017 Sequence
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c 28	58.2	2.8	346274	1	BX640443	BX640443 Bordetell
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c 30	56.6	2.8	349346	1	BX640418	BX640418 Bordetell
c 31	56.2	2.7	346510	1	AP003011	AP003011 Mesorhizo
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c 35	52.8	2.6	10896	1	AE000944	AE000944 Archaeogl
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c 37	51.2	2.5	309904	1	AB016865	AB016865 Pseudomon
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c 39	47.8	2.3	10468	1	AB011884	AB011884 Thermus t
c 40	46.8	2.3	1100000	1	AE016827_15	AE016827_15 Pseudomon
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c 44	46.2	2.3	505	6	AR219157	AR219157 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS   D90777   18554 bp   DNA   linear   BCT 29-MAY-1997
DEFINITION E.coli genomic DNA, Kohara clone #266(31.1-31.5 min.).
ACCESSION   D90777 AB001340
VERSION   D90777.1 GI:1742263
KEYWORDS   .
SOURCE   Escherichia coli
  ORGANISM Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1 (sites)
  AUTHORS   Aiba,H., Baba,T., Fujita,K., Hayashi,K., Inada,T., Isono,K.,
            Itoh,T., Kasai,H., Kashimoto,K., Kimura,S., Kitakawa,M.,
            Kitagawa,M., Makino,K., Miki,T., Mizobuchi,K., Mori,H., Mori,T.,
            Motomura,K., Nakade,S., Nakamura,Y., Nashimoto,H., Nishio,Y.,
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            Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C.,
            Yamamoto,Y., and Horiuchi,T.
  TITLE   A 570-kb DNA sequence of the Escherichia coli K-12 genome
            corresponding to the 28.0-40.1 min region on the linkage map
  JOURNAL   DNA Res. 3 (6), 363-377 (1996)
   MEDLINE   97251357
    PUBMED   9097039
REFERENCE   2 (sites)
  AUTHORS   Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
            Ikemoto,K., Inada,T., Isono,K., Kim,S., Isono,S., Itoh,T., Kanai,K.,
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            Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T.,
            Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
            Yamamoto,Y. and Yano,M.
  TITLE   The systematic sequencing of the Escherichia coli genome in Japan
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 18554)
  AUTHORS   Mori,H.
  TITLE   Direct Submission
  JOURNAL   Submitted (14-DEC-1996) Hirotada Mori, NARA Institute of Science
            and Technology, Res. & Edu. Center for Genetic Info.; 8916-5
            Takayama, Ikoma, Nara 630-01, Japan
            (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
            Fax:81-7437-2-5669)

```
COMMENT      Collaboration Information:
             Project:
                 The Japan E.coli genome DNA sequencing project
             Group:
                 The Japan E.coli genome DNA sequencing group
             Members: (1995.4 - 1996.3)
                 Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
                 Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
                 Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
                 Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
                 Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
                 Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N.,
                 Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
                 Yamamoto,Y. and Yano,M.
             Headed by:
                 Name: Takashi Horiuchi
                 Address: National Institute of Basic Biology, Okazaki, 444, Japan
                 E-mail: kishori@nibb.ac.jp
             Information operator:
                 Name: Hirotada Mori
                 Address: NARA Institute of Science and Technology,
                 Ikoma, 630-01, Japan
                 E-mail: hmori@gtc.aist-nara.ac.jp
             URL:
                 The Japan E. coli genome database
                 http:bsw3.aist-nara.ac.jp.
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Db   9080 AACTGCTGCGGTACTGGGCGGAAGCAATGTCACCCCGGGATCAACCGGAGTTTGCGCTGTTTATT 9021

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Query sequence alignment continues with paired Qy/Db rows numbered 960 through 1920 (Qy) and 8900 down to 7941 (Db).

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7940 GCAGAAGAAAAACCAACAGGTGTTGGTTGGAAATGGGCTGTGAGAGGTAATTATTCAATCAGCATCAA 7881
Qy   1981 ACCCGGTGGGCGCTGTATTCAATTCTGACGGTGAATGGGCTGTAGAGGTATTCAATCAGCATCAA 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7880 ACCCGGTGGGCGCTGTATTCAATTCTGACGGTGAATGGGCTGTAGAGGTATTCAATCAGCATCAA 7821
Qy   2041 GATTAA 2046
          ||||||
Db   7820 GATTAA 7815
```

RESULT 2
U00096_14/c
WPCOMMENT
Sequence split into 47 fragments   LOCUS U00096 Accession U00096

Fragment Name	Begin	End
U00096_00	1	110000
U00096_01	100001	210000
U00096_02	200001	310000
U00096_03	300001	410000
U00096_04	400001	510000
U00096_05	500001	610000
U00096_06	600001	710000
U00096_07	700001	810000
U00096_08	800001	910000
U00096_09	900001	1010000
U00096_10	1000001	1110000
U00096_11	1100001	1210000
U00096_12	1200001	1310000
U00096_13	1300001	1410000
U00096_14	1400001	1510000
U00096_15	1500001	1610000
U00096_16	1600001	1710000
U00096_17	1700001	1810000
U00096_18	1800001	1910000
U00096_19	1900001	2010000
U00096_20	2000001	2110000
U00096_21	2100001	2210000
U00096_22	2200001	2310000
U00096_23	2300001	2410000
U00096_24	2400001	2510000
U00096_25	2500001	2610000
U00096_26	2600001	2710000
U00096_27	2700001	2810000
U00096_28	2800001	2910000
U00096_29	2900001	3010000
U00096_30	3000001	3110000
U00096_31	3100001	3210000
U00096_32	3200001	3310000
U00096_33	3300001	3410000
U00096_34	3400001	3510000
U00096_35	3500001	3610000
U00096_36	3600001	3710000
U00096_37	3700001	3810000
U00096_38	3800001	3910000
U00096_39	3900001	4010000
U00096_40	4000001	4110000
U00096_41	4100001	4210000
U00096_42	4200001	4310000
U00096_43	4300001	4410000
U00096_44	4400001	4510000
U00096_45	4500001	4610000
U00096_46	4600001	4639675

Continuation (15 of 47) of U00096 from base 1400001 (U00096 Escherichia coli K-12 MG1655

Query Match   100.0%; Score 2046; DB 1; Length 110000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2046; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGCAGCAGTTAGCCAGTTTCTTATCGGGTACCTGGCCAGTCTGGCCGGGGCGCCGTAGCCGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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